



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/069,290
Source: PS/10
Date Processed by STIC: 3/7/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/069,290

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



PCT10

RAW SEQUENCE LISTING

DATE: 03/07/2002

PATENT APPLICATION: US/10/069,290

TIME: 15:24:35

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

Does N: J069290

Corrected? See N: J069290

2 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
W--> 3 <120> TITLE OF INVENTION: Agent for enhancing expression of HM1.24
W--> 4 comprising as an active component interferon(?) please use Western alphabetical
W--> 5 <130> FILE REFERENCE: H757 characters; otherwise,
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/069,290 CRF program translates
E--> 6 <141> CURRENT FILING DATE: 2002-02-25 as "?"
E--> 6 <160> NUMBER OF SEQ ID: (5) 25 (p3)

ERRORED SEQUENCES

W--> 7 <210> SEQ ID NO: 1
8 <211> LENGTH: (1073) 1013 shown (p.2)
9 <212> TYPE: DNA
10 <213> ORGANISM: Homosapiens
11 <223> OTHER INFORMATION: Nucleotide sequence coding for HM1.24 protein
12 antigen
W--> 13 <400> SEQUENCE: 1
14 gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc 49
15 Met Ala Ser Thr Ser Tyr Asp Tyr Cys
16 1 5
17 aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 97
18 Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
19 10 15 20 25
20 ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 145
21 Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
22 30 35 40
23 att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 193
24 Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
25 45 50 55
26 cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 241
27 Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
28 60 65 70
29 ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc 289
30 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
31 75 80 85
32 acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 337
33 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
34 90 95 100 105
35 aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 385
36 Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
37 110 115 120
38 aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 433

2237 ← insert this mandatory
numerical identifier whenever
2217, 2227, or 2237 is shown
Please edit all sequences
This is a global error

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002

TIME: 15:24:35

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

```

39 Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
40      125      130      135
41 aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac      481
42 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
43      140      145      150
44 tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg      529
45 Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
46      155      160      165
47 att gtg ctg ctg ggc ctc agc gct ctg ctg cag tga gatcccagga      575
48 Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
49 170      175      180
50 agctggcaca tcttggaagg tccgtcctgc tcggttttc gcttgaacat tcccttgatc      635
51 tcatcagttc tgagcgggtc atggggcaac acggttagcg gggagagcac ggggtagccg      695
52 gagaagggcc tctggagcag gtctggaggg gccatggggc agtcctgggt ctggggacac      755
53 agtcgggttg acccagggt gtctccctcc agagcctccc tccggacaat gagtcccccc      815
54 tcttgtctcc caccctgaga ttgggcatgg ggtgcggtgt ggggggcatg tgctgcctgt      875
55 tgttatgggt ttttttgcg gggggggttg ctttttctg ggggtcttga gctccaaaaa      935
56 aataaacact tcctttgagg gagagcacac cttaaaaaaa aaaaaaaaaa aaaaaaaaaa      995
E--> 57 aaaattcggg cggccgcc      1013
58 <210> SEQ ID NO: 3
59 <211> LENGTH: 2016 (p 3)
60 <212> TYPE: DNA
61 <213> ORGANISM: Homosapiens
62 <223> OTHER INFORMATION: Nucleotide sequence of promoter region of gene
63 coding for Hm1.24 protein antigen
64 <400> SEQUENCE: 3
65 actaaaagtc tctgatatgc agaaataatg gcataagctg tttttctgtc tgtccctctc      60
66 ctctctctct gctcgggtcg ccaggcaggg aagggtcccc tgtccagtgg acacgtgacc      120
67 cacatgacct tacctatcat tggagatgac tcacactctt taccctgccc cttttgcttt      180
68 gtatccaata aataacagca cagccagaca ttcggggcca ctaccagtct ccgcgcattg      240
69 ctggtagtgg tccccgggc ccagctgtct tttcttttat ctcttcgtct tgtgtcttta      300
70 tttctacact ctctcgtcgc cgcacacagg gagagaccca ctgaccctgt ggggctggtc      360
71 cctacagtaa ttttaaaggg aagagcaaca aactttcggg ttgcagggtt gggactgttt      420
72 acagctgcaa aatttagaga ggacatcaat ctattattat ccacatttta cagctgggga      480
73 aatcaatgct aagagaggaa attcatttgc ccagaggtgc accaccctgg cctccaatgt      540
74 gcaattcatg caattgtgat ttccgacctg gtcccaaact aacctaaaag ttagcaggcc      600
75 agaacagtgc tgctcaaata agtcagctta gtcaaataag tcaggcaaaag gtcgtgtctt      660
76 tgcacctgga gtccctggcca ggctggtagg tccctcctcc tgggacaagt tcacctcag      720
77 aattttcagc aagatcatct cccacagctt gttaattggg tcttggttct aagtgatttt      780
78 tttgtttatt ggtttaagag atgggatccc actctatcac ccaggcttga gtgccgtggc      840
79 acaatcatag ctgctgcag cctcaaaact ctgggctcga gtgatcctcc tgcctcagcc      900
80 tcccagctc agcctgggac cacaggcatg taccaccatg cctggctcta agtggcttta      960
81 atggggctct tctgagggat gttggagtca gggcctgggg ggagttcccc aggccttctg      1020
82 ggaggcctgg gctctggact tgacctcgcc tactgtctgg ccctgctgaa aagaaaaaaa      1080
83 aacatggaag tggcagacct aacagaatct gggctgtggg caggatgtgg ctgaagaagc      1140
84 cacaagaaaa acatgcagtc ccctttcagc ggtcatgccc agcagttggg tgccgataat      1200
85 ggccctgatt tctgttagga agccctggct ctcttgacca catggacagt gtctgagggt      1260
86 ggccctgtta tcccccttg cagatgaaga aacaggctca gagagtttac ctgggtatct      1320
87 ggagtcaccg gagcactttt tctggaagta ggagcttggt tctgcagggt gccaaagacag      1380

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002
TIME: 15:24:35

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\03072002\J069290.raw

118 agaccgacat tgtttgttg ctgggtcggc ctcccagttt tcagctggct ccagtctcac 1440
119 ctgttgctca cacaccctcc atgtctccca tagtcccctc ggtggggaca gaggcactgg 1500
120 atgaagccct gctcgtcacc acagagacac ctgaacacaa aaaccagtcc ctgggggtcag 1560
121 acccaggccc cgccccaga cccaggccct gccctcactc caccacgcaa ctgtgcaacc 1620
122 tcagtttccc caggtggaga ccggaccaac aatgatggcc tctgcctctt caggtcatag 1680
123 tacagatgaa tacaggctgg cagggcctag gcaactcagta acacacggca gaggcacagg 1740
124 gacttaagat ggagtgtccc aggcagccac agttggctgg caccagttg ggaagggccc 1800
125 aagggtttt aaagcagggt gaaaaaaaaa gccacacctc tttctgggaa actgaaactg 1860
126 aaaacctaat taatcctctg cctgtagggt cctcatgcaa gagctgctgg tcagagcact 1920
127 tcctggaact tgcatttggt caggacgttt cctatgctaa taaaggggtg gccgtagaa 1980
128 gattccagca cctcccccta actccaggcc agactccttt cagctaaagg ggagatctgg 2040
129 atg gca tct act tgc tat gac 2061
130 Met Ala Ser Thr Ser Tyr Asp

E-X 131 5
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 78 28 shown
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence

W-T 146 <220> FEATURE:
W-T 147 <221> NAME/KEY:
148 <222> LOCATION:
149 <223> OTHER INFORMATION: Primer BST2B

W--> 150 <400> SEQUENCE: 5

E--> 151 atagtcatac gaagtagatg ccatccag

286 <210> SEQ ID NO: 12
287 <211> LENGTH: 29
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence

W--> 290 <220> FEATURE:

W--> 291 <221> NAME/KEY:

292 <222> LOCATION:

293 <223> OTHER INFORMATION: ISRE-F2 probe

W--> 294 <400> SEQUENCE: 12

E--> 295 aatttctggg aaactgaaagtgaacacct

306 <210> SEQ ID NO: 14
307 <211> LENGTH: 37 36
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence

W-T 310 <220> FEATURE:

W-T 311 <221> NAME/KEY:

312 <222> LOCATION:

313 <223> OTHER INFORMATION: adp-1 probe

W--> 314 <400> SEQUENCE: 14

E--> 315 catggcatct acttcgtatg actattgcag agtgcc

416 <210> SEQ ID NO: 25 last sequence in file
417 <211> LENGTH: 30
418 <212> TYPE: DNA
419 <213> ORGANISM: Artificial Sequence

W-T 420 <220> FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002
TIME: 15:24:35

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\03072002\J069290.raw

W--> 421 <221> NAME/KEY:
422 <222> LOCATION:
423 <223> OTHER INFORMATION: Primer IRF2-R1
W--> 424 <400> SEQUENCE: 25
425 agtcgggtacc ttaactgctc ttgacgcggg 30
E--> 426 1/12
E--> 428 - 1 -

delete

see p 5 for more error

Please do not use bold print in the file

Per 1.823 of Sequence Rules,

"A fixed-width font should be used exclusively throughout the 'Sequence Listing'."

Do NOT change fonts

10/069, 290

5

<210> 10

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<221>

<222>

<223>

<400> 10

← all item 11 on Error Summary Sheet

FYI

100 of 1000 Xaa for 1000 amino acids
The following sequence is for
explaining the sequence of
each amino acid using the Xaa

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002

TIME: 15:24:36

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:7 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1073 Found:1013 SEQ:1
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:283 W: Missing Blank Line separator, <400> field identifier
L:131 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2016 Found:2061 SEQ:3
L:136 M:283 W: Missing Blank Line separator, <220> field identifier
L:137 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:140 M:283 W: Missing Blank Line separator, <400> field identifier
L:146 M:283 W: Missing Blank Line separator, <220> field identifier
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:150 M:283 W: Missing Blank Line separator, <400> field identifier
L:151 M:252 E: No. of Seq. differs, <211> LENGTH:Input:78 Found:28 SEQ:5
L:157 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:283 W: Missing Blank Line separator, <400> field identifier
L:248 M:283 W: Missing Blank Line separator, <220> field identifier
L:249 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:253 M:283 W: Missing Blank Line separator, <400> field identifier
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:259 M:283 W: Missing Blank Line separator, <220> field identifier
L:260 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:264 M:283 W: Missing Blank Line separator, <400> field identifier
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:270 M:283 W: Missing Blank Line separator, <220> field identifier
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:274 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:283 W: Missing Blank Line separator, <220> field identifier
L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:290 M:283 W: Missing Blank Line separator, <220> field identifier
L:291 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:294 M:283 W: Missing Blank Line separator, <400> field identifier
L:295 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:300 M:283 W: Missing Blank Line separator, <220> field identifier
L:301 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:310 M:283 W: Missing Blank Line separator, <220> field identifier
L:311 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:254 E: No. of Bases conflict, LENGTH:Input:37 Counted:36 SEQ:14
L:315 M:252 E: No. of Seq. differs, <211> LENGTH:Input:37 Found:36 SEQ:14
L:320 M:283 W: Missing Blank Line separator, <220> field identifier
L:321 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/069,290

DATE: 03/07/2002

TIME: 15:24:36

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03072002\J069290.raw

L:324 M:283 W: Missing Blank Line separator, <400> field identifier
 L:330 M:283 W: Missing Blank Line separator, <220> field identifier
 L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
 L:334 M:283 W: Missing Blank Line separator, <400> field identifier
 L:340 M:283 W: Missing Blank Line separator, <220> field identifier
 L:341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
 L:344 M:283 W: Missing Blank Line separator, <400> field identifier
 L:350 M:283 W: Missing Blank Line separator, <220> field identifier
 L:351 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
 L:354 M:283 W: Missing Blank Line separator, <400> field identifier
 L:360 M:283 W: Missing Blank Line separator, <220> field identifier
 L:361 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
 L:364 M:283 W: Missing Blank Line separator, <400> field identifier
 L:370 M:283 W: Missing Blank Line separator, <220> field identifier
 L:371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
 L:374 M:283 W: Missing Blank Line separator, <400> field identifier
 L:380 M:283 W: Missing Blank Line separator, <220> field identifier
 L:381 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
 L:384 M:283 W: Missing Blank Line separator, <400> field identifier
 L:390 M:283 W: Missing Blank Line separator, <220> field identifier
 L:391 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
 L:394 M:283 W: Missing Blank Line separator, <400> field identifier
 L:400 M:283 W: Missing Blank Line separator, <220> field identifier
 L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
 L:404 M:283 W: Missing Blank Line separator, <400> field identifier
 L:410 M:283 W: Missing Blank Line separator, <220> field identifier
 L:411 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
 L:414 M:283 W: Missing Blank Line separator, <400> field identifier
 L:420 M:283 W: Missing Blank Line separator, <220> field identifier
 L:421 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
 L:424 M:283 W: Missing Blank Line separator, <400> field identifier
 L:426 M:254 E: No. of Bases conflict, LENGTH:Input:12 Counted:31 SEQ:25
 L:426 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 M:254 Repeated in SeqNo=25
 L:428 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:31 SEQ:25
 L:6 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (5) Counted (25)